2-6

OR

2 0

Application No.: 09/471,669

Page 3

IN THE DRAWINGS:

Please replace drawing sheets 1-26 with drawing sheets 1-51.

REMARKS

Claims 1-48 and 51-113 are pending in the application. Claims 48 and 51-69 are currently under consideration, claims 49 and 50 having been canceled, and claims 1-47 and 70-113 having been withdrawn from consideration. Claims 63, 64, 67, and 68 have been amended. The amendments to claims 63, 64, 67, and 68 add no new matter to the application.

In response to the Notice of Draftsperson's Patent Drawing Review dated June 27, 2000, Applicants submit drawing sheets 1-51 to replace drawing sheets 1-26 as filed.

The Applicants note the objection to the specification and claims 51-66 made in the Office Action mailed October 22, 2001, paper No. 13 have been withdrawn. Applicants note the following rejections made in the Office Action mailed October 22, 2001, paper No. 13 have been withdrawn: the rejection of claims 62, 63, and 68 under 35 U.S.C. § 112, second paragraph; the rejection of claim 48 under 35 U.S.C. § 112, first paragraph; the rejection of claims 48 and 51-57 under 35 U.S.C. § 102; and, the rejection of claims 58-63 under 35 U.S.C. § 103(a).

Applicants believe that the cancellation of claim 50 moots the non-statutory double patenting rejection made in the Office Action mailed October 22, 2001, paper No. 13.

Objection to Claims 63, 67, and 68

Claims 63, 67, and 68 have been amended as suggested by the Examiner. Claim
63 has been amended to remove "[1-501]." Claim 67 has been amended to expand "APPwt" and
"APPsw." Claim 68 has been amended to expand "APP." The amendments to claim 63 and
claims 67-68 are wholly stylistic in nature.

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGGATGGGCGCGGGAG TGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCG CAGCGGCCTGGGGGCGCCCCCCTGGGGCTGCGGCTGCCCCGGGA GACCGACGAGGGCCCGAGGGGCCGGCCGGGGGGCAGCTTTGT GGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTAC GTGGAGATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGG CTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACATACCGGG ACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGA AGGGGAGCTGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC GTCACTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTT CTTCATCAACGGCTCCAACTGGGAAGGCATCCTGGGGCTGGCCTATG CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTG TGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCG GAGGGAGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGC AGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTATGAGGTGAT CATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCA AGGAGTACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAAC CTTCGTTTGCCCAAGAAGTGTTTGAAGCTGCAGTCAAATCCATCAAG GCAGCCTCCTCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGA GCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATTTTCC CAGTCATCTCACCTAATGGGTGAGGTTACCAACCAGTCCTTCC GCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATC CACGGCACTGTTATGGGAGCTGTTATCATGGAGGGCTTCTACGTTG TCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC CATGTGCACGATGAGTTCAGGACGCAGCGGTGGAAGGCCCTTTTG GAGTCAACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGC CCTCTTCATGCTGCCACTCTGCCTCATGGTGTCAGTGGCGCTGCC TCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCC **CTGCTGAAG**

FIG. 1A

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CCATGCCGGCCCTCACAGCCCCGCCGGGAGCCCGAGCCCGCTGCCCAGG CTGGCCGCCGCSGTGCCGATGTAGCGGGCTCCGGATCCCAGCCTCTCCCCT GCTCCCGTGCTCTGCGGATCTCCCCTGACCGCTCTCCACAGCCCGGACCCG GGGGCTGGCCCAGGCCCTGCAGGCCCTGGCGTCCTGATGCCCCCAAGCT CCCTCTCCTGAGAAGCCACCAGCACCACCCAGACTTGGGGGCAGGCGCCA GGGACGGACGTGGGCCAGTGCGAGCCCAGAGGCCCGAAGGCCGGGGCC CACCATGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAG TGCTGCCTGCCCACGCACCCAGCACGCATCCGGCTGCCCCTGCGCAGC GGCCTGGGGGCGCCCCCCTGGGGCTGCGGCTGCCCCGGGAGACCGACG AAGAGCCCGAGGAGCCCGGCCGGAGGGCAGCTTTGTGGAGATGGTGGAC AACCTGAGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACCGTGGG CAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT TGCAGTGGGTGCTGCCCCCCCCCCCTTCCTGCATCGCTACTACCAGAGGCA GCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACAC CCAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCC ATGGCCCCAACGTCACTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGA CAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTGGGGCTGGCCTAT TAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGG CATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC ATCCGGCGGGAGTGGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAAT GGACAGGATCTGAAAATGGACTGCAAGGAGTACAACTATGACAAGAGCATTG TGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGC **AGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGATGGTTTC** TGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAAC CCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGC CACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGC ACTGTTATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGG CCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTT CAGGACGCCAGCGTGGAAGGCCCTTTTGTCACCTTGGACATGGAAGACTG TGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGT GTCAGTGGCGCTGCCTGCCTGCGCAGCAGCATGATGACTTTGCTG ATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATT CCCCTGGACCACCCCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGA CTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAGGGACTGTA CCTGTAGGAAACAGAAAGAGAAGAAGAAGCACTCTGCTGGCGGGAATAC TCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCC CTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTT TCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCC CTGTGGTACCCTGGCAGAGAGAGACCAAGCTTGTTTCCCTGCTGGCCAAA GTCAGTAGGAGAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGT ATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGAATT

FIG. 1B

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MAQALPWLLLWMGAGVLPAHGTQHGIRLPLRSGLGGAPLGLRL
PRETDEEPEEPGRRGSFVEMVDNLRGKSGQGYYVEMTVGSPP
QTLNILVDTGSSNFAVGAAPHPFLHRYYQRQLSSTYRDLRKGVY
VPYTQGKWEGELGTDLVSIPHGPNVTVRANIAAITESDKFFINGS
NWEGILGLAYAEIARPDDSLEPFFDSLVKQTHVPNLFSLQLCGAG
FPLNQSEVLASVGGSMIIGGIDHSLYTGSLWYTPIRREWYYEVIIV
RVEINGQDLKMDCKEYNYDKSIVDSGTTNLRLPKKVFEAAVKSIK
AASSTEKFPDGFWLGEQLVCWQAGTTPWNIFPVISLYLMGEVTN
QSFRITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIM
EGFYVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDC
GYNIPQTDESTLMTIAYVMAAICALFMLPLCLMVCQWRCLRCLR
QQHDDFADDISLLK

FIG. 2A

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ETDEEPEEPGRRGSFVEMVDNLRGKSGQGYYVEMTVGSPPQT
LNILVDTGSSNFAVGAAPHPFLHRYYQRQLSSTYRDLRKGVYVP
YTQGKWEGELGTDLVSIPHGPNVTVRANIAAITESDKFFINGSNW
EGILGLAYAEIARPDDSLEPFFDSLVKQTHVPNLFSLQLCGAGFP
LNQSEVLASVGGSMIIGGIDHSLYTGSLWYTPIRREWYYEVIIVRV
EINGQDLKMDCKEYNYDKSIVDSGTTNLRLPKKVFEAAVKSIKAA
SSTEKFPDGFWLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQ
SFRITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIME
GFYVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDC
GYNIPQTDESTLMTIAYVMAAICALFMLPLCLMVCQWRCLRCLR
QQHDDFADDISLLK

FIG. 2B

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MAQALPWLLLWMGAGVLPAHGTQHGIRLPLRSGLGGAPLGLRL PRETDEEPEEPGRRGSFVEMVDNLRGKSGQGYYVEMTVGSPP QTLNILVDTGSSNFAVGAAPHPFLHRYYQRQLSSTYRDLRKGVY VPYTQGKWEGELGTDLVSIPHGPNVTVRANIAAITESDKFFINGS NWEGILGLAYAEIARPDDSLEPFFDSLVKQTHVPNLFSLQLCGAG FPLNQSEVLASVGGSMIIGGIDHSLYTGSLWYTPIRREWYYEVIIV RVEINGQDLKMDCKEYNYDKSIVDSGTTNLRLPKKVFEAAVKSIK AASSTEKFPDGFWLGEQLVCWQAGTTPWNIFPVISLYLMGEVTN QSFRITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIM EGFYVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDC GYNIPQTDEDYKDDDDK

FIG. 3A

ETDEEPEEPGRRGSFVEMVDNLRGKSGQGYYVEMTVGSPPQT
LNILVDTGSSNFAVGAAPHPFLHRYYQRQLSSTYRDLRKGVYVP
YTQGKWEGELGTDLVSIPHGPNVTVRANIAAITESDKFFINGSNW
EGILGLAYAEIARPDDSLEPFFDSLVKQTHVPNLFSLQLCGAGFP
LNQSEVLASVGGSMIIGGIDHSLYTGSLWYTPIRREWYYEVIIVRV
EINGQDLKMDCKEYNYDKSIVDSGTTNLRLPKKVFEAAVKSIKAA
SSTEKFPDGFWLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQ
SFRITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIME
GFYVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDC
GYNIPQTDEDYKDDDDK

FIG. 3B

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NH2-K-T-E-E-I-S-E-V-N-Sta-V-A-E-F-COOH

Fig. 4



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192 192 194 195 195 195 195 195 195 195 195 195 195	
tac Sein Aga Aga Aga Lac	Tyr
जिल्हा । जिल्हा । संव अर्थ । विच । जिल्हा ।	Arg
, , , , , , , , , , , , , , , , , , ,	His 110
ggc cgg Arg Afs at gat yal yal	Leu
क्रम व्रव्य वर्ष वर्ष वर्ष वर्ष	Phe
tgg at Trp Me cgg ct Arg Le agc tt Ser Ph tac ta Tyr Ty 75 ccg gt	Pro
	His
ctg Leu Leu Ctg Gly 255 Arg Arg Gln Gln Gln Gln Cag Gln Gln Cag	Pro 105
	Ala
	Ala
ccc tgg Pro Trp S acc cag Thr Gln Pro Leu Ccc ggc Pro Gly Pro Gly Ntel Aag tcg Cag acg Gln Thr	Gly
ctg leu 5 5 6 1 y	Val
gac agg agg agg agg agg agg agg agg agg	Ala 100
cc caa gcc la Gln Ala ct gcc cac cot gcc cac cu ggg ggg eu Gly Gly 35 35 36 36 37 38 38 38 39 39 39 39 39 30 30 30 30 30 30 30 30 30 30 30 30 30	Phe
ਲਕ ਪਰ ਪਜ ਲਹਾ ਕਕ ਵਿੱਹਿਨ ਕ	Asn
agt agt	Ser

Fig. 5A



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384	432	480	528	576	624	672
gtg Val	gac Asp	att Ile 160	tgg Trp	gac Asp	GGG	tac cag tsn Gln N-glycos
ggt Gly	acc Thr	aac Asn	aac Asn 175	gac Asp	gtt Val	0 A
аад Lys	ggc Gly	gcc Ala	Ser	cct Pro 190	cac His	ctc Leu
cgg Arg 125	ctg Leu	cgt Arg	ac ggc sn Gly N-glycos	agg Arg	acc Thr 205	Pro
ctc Leu	gag Glu 140	gtg Val	ğ K	gcc Ala	cag Gln	ttc Phe 220
gac Asp	ggg Gl $_{ m Y}$	act Thr 155	atc Ile	att Ile	aag Lys	ggc
cgg Arg	gaa Glu	c gtc n Val N-glycos	ttc Phe 170	gag Glu	gta Val	gct Ala
tac Tyr	tgg Trp	As	ttc Phe	gct Ala 185	ctg Leu	ggt Gly
aca Thr 120	aag Lys	Pro	аад Lys	tat Tyr	tct Ser 200	tgt Cys
agc Ser	99c Gly 135	99c G1 <u>Y</u>	gac Asp	gcc Ala	gac Asp	ctt Leu 215
tac Ser	cag Gln	cat His 150	tca Ser	ctg Leu	ttt Phe	cag Gln
ctg Leu	acc Thr	Pro	gaa Glu 165	999 G1 <u>y</u>	ttc Phe	ctg Leu
cag Gln	tac Tyr	atc Ile	act Thr	ctg Leu 180	cct Pro	Ser
agg Arg 115	CCC	agc Ser	atc Ile	atc Ile	gag Glu 195	ttc Phe
cag Gln	gtg Val 130	gta Val	gcc Ala	ggc Gly	ctg Leu	ctc Leu 210
tac Tyr	tat Tyr	ctg Leu 145	gct Ala	gaa Glu	tec Ser	aac Asn

Fig. 5B



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						œ
720	768	816	864	912	096	1008
atc Ile 240	cgg Arg	cag Gln	gtg Val	gct Ala	gat Asp 320	acc Thr
ggt Gly	cgg Arg 255	gga Gly	att Ile	gaa Glu	cct Pro	acc Thr 335
gga Gly	atc Ile	aat Asn 270	agc Ser	ttt Phe	ttc Phe	ggc Gly
att Ile	ccc Pro	atc Ile	aag Lys 285	gtg Val	aag Lys	gca Ala
atc Ile	aca Thr	gag Glu	gac Asp	aaa Lys 300	gag Glu	caa Gln
atg Met 235	tat Tyr	gtg Val	tat Tyr	аад Lyв	acg Thr 315	tgg Trp
agc Ser	tgg Trp 250	cgg Arg	aac Asn	Pro	tcc Ser	tgc Cys 330
$^{\rm ggg}_{\rm G1Y}$	ctc Leu	gtg Val 265	tac Tyr	ttg Leu	tcc Ser	gtg Val
gga Gly	agt Ser	att Ile	gag G1u 280	cgt Arg	gcc Ala	ctg Leu
gtc Val	ggc Gly	atc Ile	aag Lys	ctt Leu 295	gca Ala	cag Gln
tct Ser 230	aca Thr	gtg Val	tgc Cys	aac Asn	aag Lys 310	gag Glu
gcc Ala	tac Tyr 245	gag Glu	gac Asp	acc Thr	atc Ile	gga G1 <u>y</u> 325
ctg Leu	ctg Leu	tat Tyr 260	atg Met	acc Thr	tcc	cta Leu
gtg Val	teg Ser	tat Tyr	aaa Lys 275	gt ggc er Gly 90 Active-D	ааа Lys	tgg Trp
gaa Glu	cac His	tgg Trp	ctg Leu	4 00 00	gtc Val	ttc Phe
tct Ser 225 N-gly	gac Asp	gag Glu	gat Asp	gac	gca Ala 305	ggt Gly

Fig. 5C



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Internal peptide sequence

1056	1104	1152	1200	1248	1296
gtt Val	cgg	gcc Ala	gag Glu 400	gct Ala	gaa Glu
gag Glu	ctg Leu	ttt Phe	atg Met	ttt Phe	gtg Val
ggt Gly 350	tac Tyr	аад Lys	atc Ile	ggc Gly	gcg Ala 430
atg Met	caa Gln 365	tac Tyr	gtt Val	att	gca Ala
cta Leu	cag Gln	tgt Cys 380	gct Ala	cga Arg	acg Thr
tac Tyr	ccg Pro	gас Авр	gga G1Y 395	ааа Lys	agg Arg
ctc Leu	ctt Leu	gас Авр	atg Met	cga Arg 410	ttc Phe
tca Ser 345	atc Ile	caa Gln	gtt Val	gcc Ala	gag Glu 425
atc Ile	acc Thr 360	tac Ser	act Thr	cgg Arg	gat Asp
gtc Val	atc Ile	acg Thr 375	ggc Gly	gat Asp	cac His
cca Pro	cgc Arg	gcc Ala	acg Thr 390	ttt Phe	gtg Val
ttc Phe	ttc Phe	gtg Val	tcc Ser	gtc Val 405	cat His
att Ile 340	Ser	gat	tca Ser	gtt Val	tgc Cys 420
aac Asn	cag Gln 355	n-glycos cg gaa .1 Glu 0	cag Gln	tac Tyr	gct Ala
tgg Trp	Asn	gtg Val 370	tca Ser	ttc Phe	agc Ser
cct Pro	acc Thr	GCa	atc Ile 385	ggc G1у	gtc Val
Ω					

Fig. 5D



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1344	1392		1440		1488	1506
cca Pro	gcc Ala		tgg Trp 480		gac Asp	
att Ile	gct Ala		cag Gln		gat Asp 495	
aac Asn	atg Met		tgt Cys		ttt gct Phe Ala	
tac Tyr 445	gtc Val		atg gtg tgt cag Met Val Cys Gln		ttt Phe	
ggc Gly	tat Tyr 460	Transmembrane	atg Met		gac Asp 1	
tgt Cys	gcc Ala	ısmen	tgc ctc Cys Leu 475		gat Asp	
gac Asp	ata Ile	Tra	tgc Cys	orane	cat His 490	
gaa Glu	acc Thr		cca ctc Pro Leu	Transmembrane	cag Gln	
atg Met 440	atg Met		cca Pro	Trans	cag Gln	
gac Asp	ctc Leu 455		ctg Leu		aga Arg	
ttg Leu	acc Thr		atg Met 470		ctg Leu	tga
acc Thr	tca Ser		ttc Phe		tgc ctg Cys Leu 485	аад Lys
gtc Val	gag Glu		ctc Leu		cgc Arg	ctg Leu 500
ttt Phe 435	gat Asp		gcc Ala		ctc Leu	ctg Leu
cct	aca Thr 450		tgc Cys		tgc Cys	toc Ser
ggc Gly	cag Gln		atc Ile 465		cgc Arg	atc Ile

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Fig. 5E



SS Y TO SING SECTION Fraction Fraction

REDUCING (+BME)

NONREDUCING (NOME)

Fig. 6a

Fig. 6b



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Fig. 7

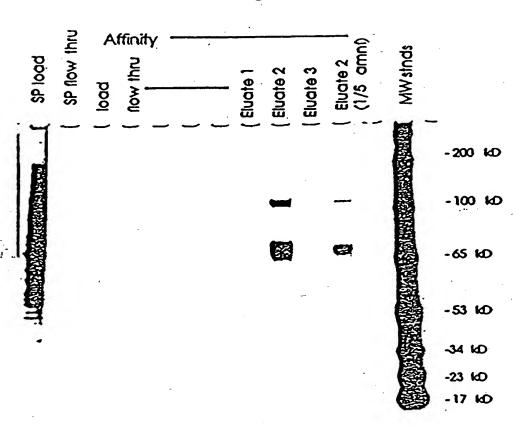


Fig. 8

1		Affinity					g
SP flow th	SP load	poo o	Flow thru	Eluate 1	Eluate 2	Eluate 3	293T stando



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GARACNGAYGARGARCCNGANGNMGNMGNGGNwSNTTYGTNGAYAAY 63

3427-3430
5' primer set 1

3448-3451
5' primer set 2

3452-3455

5' primer set 2

1° HNC/primer set 1

(3428+3433)
54 bp product

72 bp product

sequence:

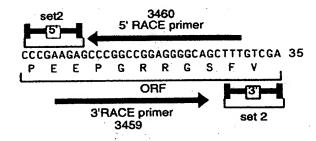


Fig. 9



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Σ	×	1	×	1	1	Н	×	1	×	1	1	口	П	Ы	Ц		Ы
	pBS/MuImPain E17 #11 cons	pBS/MuImPain E17 #14 cons	pBS/MuImPain E17 Brain#17cons	Brain#15cons	cons	•	pBS/MuImPain E17 #11 cons	pBS/MuImPain E17 #14 cons	pBS/MuImPain El7 Brain#17cons	Brain#15cons	cons		E17 #11 cons	E17 #14 cons	E17 Brain#17cons	Brain#15cons	cons
ď	17	17	[]	[]	‡3	ď	[]	[]	17	E17	#3	ģ	17	17	17	E17	#3
Human Impain Seq.	ы	Ы	ы	pBS/MuImPain E17	pBS/MuImPain H#3	Human Impain Seq.	回	回	凹	ы	pBS/MuImPain H#3	Human Impain Seg.	団	ы	ш	ш	pBS/MuImPain H#3
in	in	in	in	in	in	in	in	in	in	in	in	in	in	in	in	in	in
pa	Ра	Pa	Pa	Pa	Ра	pa	Ра	Pa	Ра	Pa	Ра	pa	Pa	Ра	Ра	Pa	Ра
IΠ	Im	Im	Im	Im	,m,	Imj	Ī	Im	Im	Im	Im	Imi	Im	Ιm	Π	II	Ш
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Brain#15cons E17 E17 pBS/MuImPain pBS/MuImPain

cons H#3 pBS/MuImPain FIG. 10D

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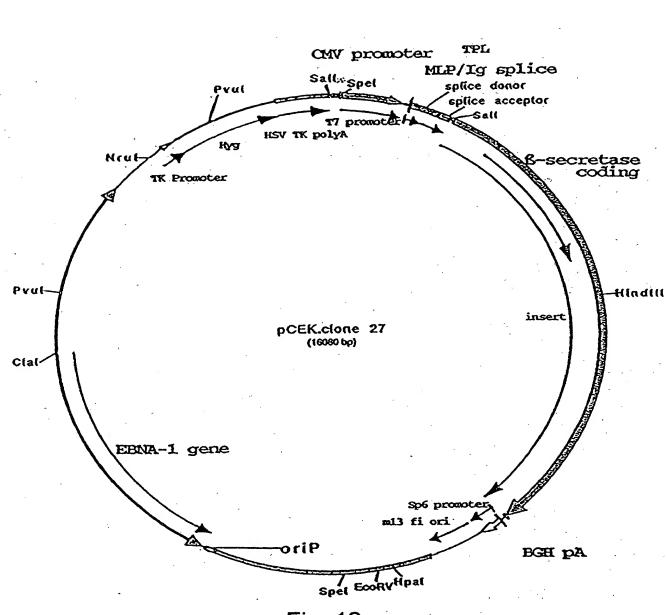


Fig. 12



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099	atgggcggta	attgacgcaa	acteegeeee	tgtcgtaaca	ctttccaaaa	atcaacggga
009	tggcaccaaa	acgtcaatgg gagtttgttt	acgtcaatgg	cacccattg	tccaagtctc	cacggggatt
540	cggtttgact	gcgtggatag	acatcaatgg	ttttggcagt	ggtgatgcgg	ctattaccat
480	ttagtcatcg	catctacgta	cttggcagta	gactttccta	gaccttatgg	cccagtacat
420	tggcattatg	atggcccgcc	atgacggtaa	attgacgtca	tacgccccct	atatgccaag
360	caagtgtatc	ggcagtacat	ctgcccactt	ttacggtaaa	ggtggactat	gacgtcaatg
300		ccatagtaac gccaataggg actttccatt	ccatagtaac	acgtatgttc	gtcaataatg	gcccattgac
240	aacgacccc	ctgaccgccc	acggtaaatg gcccgcctgg ctgaccgccc	acggtaaatg	tacataactt	agttccgcgt
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cat His 110	aag Lys	ggc Gly	gcc Ala	tcc Ser	cct Pro 190	cac His
ctg Leu	cgg Arg 125	ctg Leu	cgt Arg	ggc Gly	agg Arg	acc Thr 205
ttc Phe	ctc Leu	gag Glu 140	gtg Val	aac Asn	gcc Ala	cag Gln
ccc Pro	gac Asp	999 Gly	act Thr 155	atc Ile	att Ile	aag Lys
cac His	cgg Arg	gaa Glu	gtc Val	ttc Phe 170	gag Glu	gta Val
ccc Pro 105	tac Tyr	tgg Trp	aac Asn	ttc Phe	gct Ala 185	ctg Leu
gcc Ala	aca Thr 120	aag Lys	CCC	аад Гув	tat Tyr	tct Ser 200
gct Ala	agc Ser	ggc Gly 135	ggc Gly	gac Asp	gcc Ala	gac Asp
ggt Gly	tcc Ser	cag Gln	cat His 150	tca Ser	ctg Leu	ttt Phe
gtg Val	ctg Leu	acc Thr	GGG Pro	gaa Glu 165	999 G1y	ttc Phe
13D gca Ala 100	cag Gln	tac Tyr	atc Ile	act Thr	ctg Leu 180	cct Pro
e t	agg Arg 115	GGG	agc Ser	atc Ile	atc Ile	gag Glu 195
Figure aac tt Asn Ph	cag Gln	gtg Val 130	gta Val	gcc Ala	ggc	ctg Leu

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tct Ser 225	gac	gag Glu	gat	gac	gca Ala 305	ggt Gly
cag Gln	atc Ile 240	cgg Arg	cag Gln	gtg Val	gct Ala	gat Asp 320
aac Asn	ggt Gly	cgg Arg 255	gga Gly	att	gaa Glu	cct Pro
ctc Leu	gga Gly	atc Ile	aat Asn 270	agc	ttt Phe	ttc Phe
GCC	att Ile	ccc Pro	atc Ile	aag Lys 285	gtg Val	aag Lys
ttc Phe 220	atc Ile	aca Thr	gag Glu	gac Asp	aaa Lys 300	gag Glu
ggc Gly	atg Met 235	tat Tyr	gtg Val	tat Tyr	aag Lys	acg Thr 315
gct Ala	agc Ser	tgg Trp 250	cgg Arg	aac Asn	GGG	tcc Ser
ggt Gly	999 G1y	ctc Leu	gtg Val 265	tac Tyr	ttg Leu	tcc Ser
tgt Cys	gga Gly	agt Ser	att Ile	gag Glu 280	cgt Arg	gcc Ala
ctt Leu 215	gtc Val	ggc Gly	atc	aag Lys	ctt Leu 295	gca Ala
cag Gln	tct Ser 230	aca Thr	gtc Val	tgc Cys	aac Asn	aag Lys 310
ctg Leu	gcc Ala	tac Tyr 245	gag Glu	gac Asp	acc Thr	atc Ile
Ser Ser	ctg Leu	ctg Leu	tat Tyr 260	atg Met	acc Thr	tcc Ser
Figure 13E ctc ttc tc Leu Phe Se 210	gtg Val	teg Ser	tat Tyr	aaa Lys 275	ggc Gly	aaa Lys
Figu ctc Leu 210	gaa Glu	cac	tgg Trp	ctg	agt Ser 290	gtc Val





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2685	2733	2781	2829	2877	2925	2973
cct	acc	GCa	atc Ile 385	ggc Gly	gtc Val	ggc Gly
acc Thr	gtt Val	cgg Arg	gcc	gag Glu 400	gct Ala	gaa Glu
acc Thr 335	gag Glu	ctg Leu	ttt Phe	atg Met	ttt Phe 415	gtg Val
ggc Gly	ggt Gly 350	tac Tyr	aag Lys	atc Ile	ggc Gly	gcg Ala 430
gca Ala	atg Met	caa Gln 365	tac Tyr	gtt Val	att Ile	gca Ala
caa Gln	cta Leu	cag Gln	tgt Cys 380	gct Ala	cga Arg	acg Thr
tgg Trp	tac Tyr	ccg Pro	gac	gga G1 <u>y</u> 395	ааа Lys	agg Arg
tgc Cys 330	ctc Leu	ctt Leu	gac	atg Met	cga Arg 410	ttc Phe
gtg Val	tca Ser 345	atc Ile	caa Gln	gtt Val	gcc Ala	gag Glu 425
ctg Leu	atc Ile	acc Thr 360	ser	act Thr	agg Arg	gat Asp
cag Gln	gtc Val	atc Ile	acg Thr 375	ggc Gly	gat Asp	cac His
gag Glu	cca Pro	cgc Arg	gcc Ala	acg Thr 390	ttt Phe	gtg Val
gga G1y 325	ttc Phe	ttc Phe	gtg Val	tac Ser	gtc Val 405	cat His
13F cta Leu	att Ile 340	Ser	gat Asp	tca Ser	gtt Val	tgc Cys 420
1 p d	aac Asn	cag Gln 355	gaa Glu	cag Gln	tac Tyr	gct Ala
Figure ttc tg Phe Tr	tgg Trp	aac Asn	gtg Val 370	Ser	ttc Phe	agc Ser



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3021	3069	3117	3165	3220	3280	3340	3400	3460
ac atg gaa gac tgt ggc tac aac att cca cag 3021 sp Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln 440	tc atg acc ata gcc tat gtc atg gct gcc atc 3069 eu Met Thr Ile Ala Tyr Val Met Ala Ala Ile 55 465	tg cca ctc tgc ctc atg gtg tgt cag tgg cgc 3117 eu Pro Leu Cys Leu Met Val Cys Gln Trp Arg 475	gc cag cat gat gac ttt gct gat gac atc 3165 rg Gln Gln His Asp Asp Phe Ala Asp Asp Ile 490	ggaggcccat gggcagaaga tagagattcc cctggaccac 3220	tcacaagtag gagacacaga tggcacctgt ggccagagca	accaaatgcc tctgccttga tggagaagga aaaggctggc	tacctgtagg aaacagaaaa gagaagaaag aagcactctg	cacctcaaat ttaagtcggg aaattctgct gcttgaaact 3460
acc ttg gac Thr Leu Asp	tca acc ctc Ser Thr Leu 455	ttc atg ctg Phe Met Leu 470	tgc ctg cgc Cys Leu Arg 485	aag tga gga Lys	ttcactttgg	ctccccaccc	ccagggactg	tactcttggt
Figure 13G cct ttt gtc a Pro Phe Val 7	aca gat gag t Thr Asp Glu 3 450	tgc gcc ctc Cys Ala Leu I	tgc ctc cgc Cys Leu Arg (tcc ctg ctg Ser Leu Leu 500	acctccgtgg t	cctcaggacc c	aaggtgggtt c	ctggcgggaa t



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Figure 13I

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gccattccaa	aggggagacg	actcaatggt	gtaagacgac	attgtggaat	agcaagggca	9940
gttcctcgcc	ttaggttgta	aagggaggtc	ttactacctc	catatacgaa	cacaccggcg	10000
acccaagttc	cttcgtcggt	agtcctttct	acgtgactcc	tagccaggag	agctcttaaa	10060
ccttctgcaa	tgttctcaaa	tttcgggttg	gaacctcctt	gaccacgatg	ctttccaaac	10120
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Figure 130





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cctccactac ctcctcgacc	ccggcctcca	ctgcctcctc	gaccccggcc	tecacetect	10540
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11740 11800 11860 11380 11500 11560 11620 11680 11080 11140 11200 11260 11320 11440 tectgeceee tecaacagee ececeacet cateceette atggtcgctg tcagacagat ccaggtctga aaattcccca tcctccgaac catcctcgtc attactogoa gocoggaaaa ctocogotga acatootoaa gatttgogto ctgagcetea agecaggeet caaatteete gteeeettt ttgetggaeg gtagggatgg ggattetegg gaccettet etteetete aaggteacea gacagagatg etaetgggge gecettectg ecettectge ectectgee ettectectg etectgeece tectectget cetgececte etectgetee tgecectect gecectecte etgetectge ecetectect cetgececte etgetectge eceteceget ectgetectg etectgttee accgtgggte taaaagagat caatagacat ctttattaga cgacgctcag cettiggage caatgeaact iggaegitti iggggietee ggaeaceate ietaigieti ctgagccgcc cgggggctcct ggtcttccgc ctcctcgtcc tcgtcctctt cocogtocto gtocatggtt atcaccoct cttctttgag gtocactgco googgagoot tetggtecag atgtgtetee etteteteet aggecattte caggteetgt acetggeeee getectgece etectgecee tectgeceet ectectgete etgeceetee tectgeteet tgattcacac tgaatacagg gagtgcagac ggccctgatc tcgtcagaca ctcatcacca

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Figure 130



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Figure 13S

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13540 13060 13120 13180 13360 12820 12880 gaacgaccta caccgaactg ggcaacaatt aatagactgg gatcttcttg agatcctttt ggtggtttgt cagagcgcag gaactctgta cagtggcgat gcagcggtcg ttggtaactg ttaatttaaa ggcaactatg ctcatgacca aaatccctta acgtgagttt tggctggttt gtatcattgc agcactgggg tggctgctgc cccttccggc ggtgcctcac tgattaagca tttactcata tatactttag attgatttaa aacttcattt accacttcaa aaaaaaccac cgctaccagc ccgaaggtaa ctggcttcag cgatagttac cggataaggc tatcgtagtt atctacacga cggggagtca ctgttaccag agcttggagc agtgtagccg tagttaggcc ctagcttccc ctgcgctcgg gggtctcgcg aagatcaaag actacttact ttttgataat cccgtagaa tctgctaatc ggggttcgtg cacacagccc aggaccactt cgctgagata aactcttttt ggactcaaga cttgcaaaca cggtgagcgt taactggcga atagacagat gagcgtcaga ctgtccttct catacctcgc ttaccgggtt aatctggagc agccctcccg tgaagatcct taatctgctg ataaagttgc aagagctacc atggaggcgg attgctgata gatgaacgaa ataccaaata ggctgaacgg cgcaaactat tcagaccaag tegttecact



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14380 14140 14200 14260 13780 13960 14020 14080 13600 13660 gctgtccctg tttgctggcg gtgtccccgg aagaaatata tttgcatgtc tttagttcta tgatgacaca gcgatggata ttggctccaa cggcgcctac tgacgatcag cgatgccgcc acgccagcaa tccaggggga ctgcttcatc cccgtggccc gttgctcgcg aaaggcggac gcgtcgattt ggccttttta tcgaggtggc cgagggagct caagaattga gatccttgaa gaggaataa catccagcct cgcgtcgcga tctgacttga ccagcaacgc tccattcagg gaggcagaca aggtataggg cgaggcggca taaatcgccg ccgaagggag gatggcggac ggagagcgca cagttctccg gaagaagat agccgcgagc ggcctgcaac tttcgccacc tggaaaaacg gccacgcttc ggctgctgga gcggagccta tgcgcattca atgtgctcgc tggacagcat tcctgtcggg ggctggtaag tggggaaggc ccgccatgcc atgagaaagc ggtcggaaca cgccgcgtgc ttagcgaggt gcaacgcggg agggttggtt tctacctgcc agaatcataa agcgcgtcgg ccttttgctg ggtgaatccg aacccgttcc atcgaagtta agcgtgagct atctttatag gcaccgcgac taagcggcag cgtcaggggg aacgcctggt cggttcctgg ccggctccat aatccatgcc gacgtagccc aggtatccgg Figure 13T





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ccgagcgacc	atg	٥l			_14800	14860	14920	14980	15040	15100	15160	15220
ccga	atgagatatg	gttcgacagc	cttcgatgta	caaagatcgt	ttgacattgg	tcacgttgca	ccatggatgc	cgcaaggaat	atgtgtatca	tcgatgagct	atttcggctc	gcgaggcgat
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Figure 13V gttcggggat	tcccaatacg	aggtcgccaa	catcttcttc	tggaggccgt	ggttggcggg	15280
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gataagggag	tatatgctcc	gcattggtct	tgaccaactc	tatcagagct	tggttgacgg	15400
caatttcgat	gatgcagctt	gggcgcaggg	tcgatgcgac	gcaatcgtcc	gatccggagc	15460
cgggactgtc	gggcgtacac	aaatcgcccg	cagaagcgcg	gccgtctgga	ccgatggctg	15520
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cgggcgtctg	tggctgccaa	acacccccga	cccccaaaaa	ccaccgcgcg	gatttctggc	16060



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SalI gtgccaagct agtcgaccaa Figure 13W



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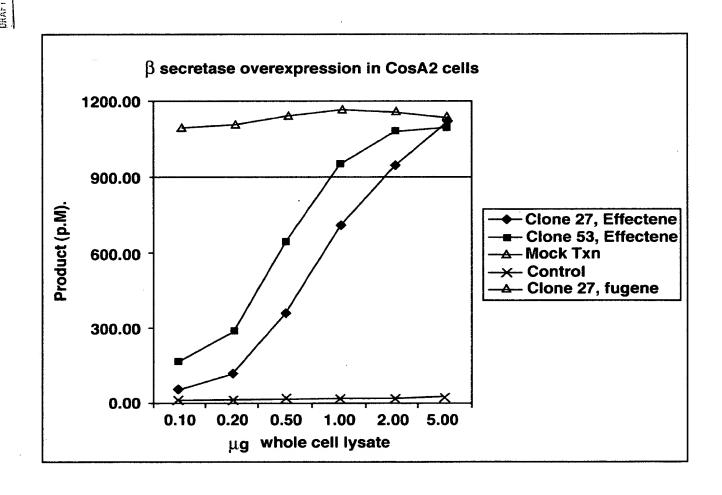


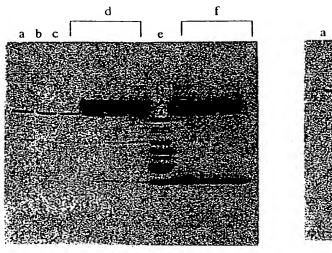
Fig. 14



ALPHOVED 1. 1. 16. T. SUBCLASS

BY 1. 1. 1. 1. SUBCLASS

RAFTSHAH 435 1226



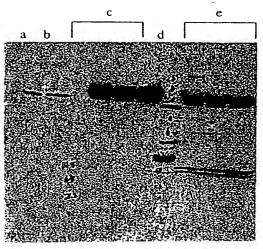


FIG. 15A

FIG. 15B



BY USSIDELASS
BRAFTSHAM, 435 | 226

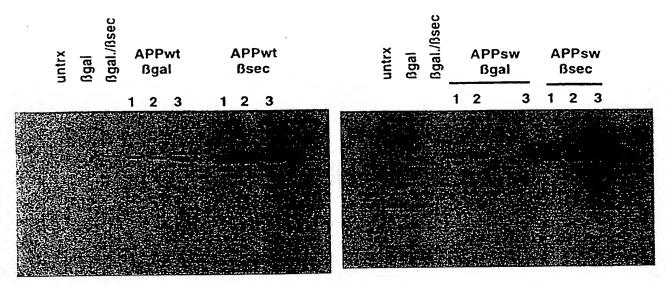


FIG. 16A

FIG. 16**B**



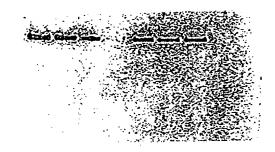
1.9	ESS SUBCLASS	435, 226
APPROVEC	84	DRAFTSMAR

APPwt APPwt

Bgal Bsec

1 2 3 1 2 3

APPsw APPsw Bgal Bsec C 1 2 3 1 2 3



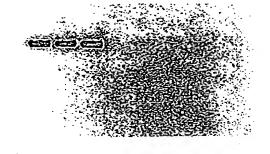


FIG. 17A

FIG. 17B





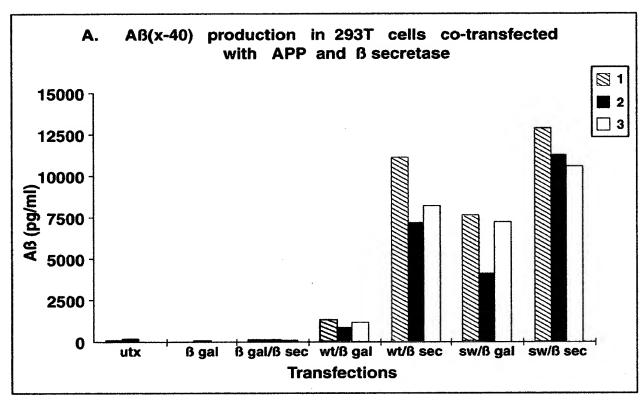


Fig. 18





	APP C-12	25
nabp	VIIIXIIIIIIIIIII	
	β-secre	etase
		APP_C-99
 anti-MBP capture	192+ve biotiny 1-	SW-192 reporter

Wild-Type Sequence Swedish SequenceVa I-Lys-Met-Asp...Va I-Asn-Leu-Asp...

Fig. 19



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Sign Sign Sign Sign Sign Sign Sign Sign	100.070	
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	APP 638	•
[38]		
APPADVING DY DRAFISION		β-secretase
	8E5	Aβ
•	192 1 ve	·
Į		
	Detected by: 1. SW192 Western Blot 2. 8E5-192 ELISA	
	Wild-Type Sequence Swedish Sequence	Val-Lys-Met-Asp Val-Asn-Leu-Asp

Fig. 20





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AFFRONS SUBSTANS ORAFISHED H 35 2 22

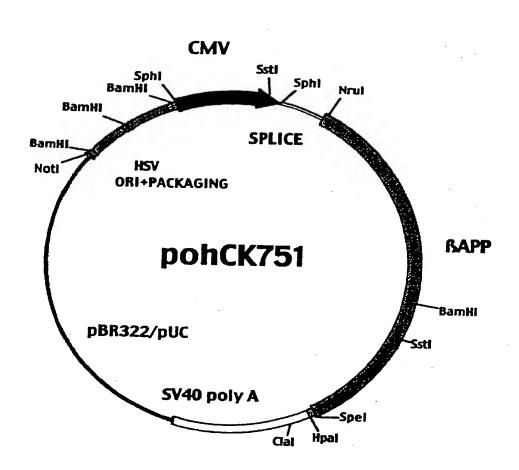


FIG. 21